

CLAIMS:

1. A method of increasing an animal population's average genetic merit, comprising;
 - a. selecting one or more traits for which an improved genetic merit is desired;
 - b. selecting one or more quantitative trait locus (QTL) for each selected trait;
 - c. selecting three or more molecular genetic markers of interest for each QTL for each selected trait;
 - d. providing databases comprising:
 - i. genotype data for three or more molecular genetic markers for each selected trait, for a plurality of animals in the population;
 - ii. data providing the pedigree for each animal in the population;
 - iii. optionally, data for one or more fixed effects;
 - e. using a computer program capable of performing a marker assisted best linear unbiased prediction to simultaneously analyze the data from the provided databases to calculate a ranking of the animals; wherein the animals are ranked according to their estimated breeding value (EBV) for the selected molecular genetic markers and, if provided, quantitative traits.
2. The method of 1 further comprising using the calculated EBVs to prepare a breeding plan for the animal population that provides for optimal improvement in the genetic merit of the population.
3. The method of claim 1 wherein the animal population is a swine herd.
4. The method of claim 1 wherein the trait is selected from the group consisting of: efficient growth traits, meat quality traits, reproduction traits, and health traits.
5. The method of claim 1 wherein the molecular genetic markers are selected from any polymorphism known to affect expression of the mRNA or protein from a gene.
6. The method of claim 5 where the polymorphism is selected from the group consisting of: single nucleotide polymorphisms, simple sequence repeats, protein point mutations, and gene isoforms.
7. The method of claim 3 wherein at least one molecular genetic marker is selected from those markers known to modulate a favorable phenotype.

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8. The method of claim 3 wherein at least one of the molecular genetic markers is a marker for selected from the group consisting of: a single nucleotide polymorphism in the porcine PRKAG3 (protein kinase, AMP-activated gamma-3 subunit) gene, and a polymorphism in the porcine melanocortin-4-receptor.
9. The method of claim 3 wherein at least one of the molecular genetic markers is a marker for a single nucleotide polymorphism in the porcine PRKAG3 gene.
10. The method of claim 1 wherein the computer program uses an iteration-on-data (IOD) algorithm and a preconditioned conjugate gradient (PCCG) algorithm to determine the animals' ranks.
11. The method of claim 10 wherein the PCCG algorithm is a variable-size block-diagonal preconditioning algorithm.
12. The method of claim 1 wherein the output of the computer program further comprises results that indicate the informativeness of one or more of the selected molecular genetic marker for at least one quantitative trait locus (QTL) and/or a calculation of the genetic closeness/proximity of one or more molecular markers to at least one QTL.
13. The method of claim 12 wherein the molecular genetic markers having the highest degree of informativeness and/or closeness for at least one QTL are identified.
14. The method of claim 1 wherein the computer program utilizes a scripting feature to improve the ease of user interface.
15. The method of claim 1 wherein the selected molecular genetic markers comprise a marker haplotype.
16. A system for increasing an animal population's average genetic merit for at one or more selected traits, the system comprising:
 - a. a computer;
 - b. a computer accessible database providing data on one or more quantitative trait locus (QTL) for each selected trait;

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- c. a computer accessible database providing data, for animals in population, for three or more molecular genetic markers for each selected QTL for each selected trait;
 - d. a computer accessible database providing pedigree data for animals in the population;
 - e. optionally, a computer accessible database providing individual data for each animal in the population for at least one fixed effect;
 - f. a computer executable program capable of simultaneously evaluating the data in all databases and ranking the animals in the population according to their respective estimated breeding value for each of the selected traits;
 - g. a user interface including a data entry system, said user interface coupled to said computer and configured to allow the user to instruct the computer to access the available databases and use the computer program to generate output that includes a ranking of the animals according to their estimated breeding values and/or their individual estimated breeding values.
17. The system of claim 16 wherein the animal population is a swine herd.
18. The system of claim 17 wherein at least one of the molecular genetic markers is selected from the group consisting of markers for the porcine PRKAG3 gene and the gene encoding the melanocortin-4-receptor.
19. The system of claim 17 wherein at least one of the molecular genetic markers is a marker for a single nucleotide polymorphism in the porcine PRKAG3 gene.
20. The system of claim 17 wherein the selected molecular genetic markers comprise a marker haplotype.
21. A system for identifying the molecular genetic marker(s) having the highest degree of informativeness for one or more selected quantitative trait locus (QTL), the system comprising:
- a. a computer;
 - b. a computer accessible database providing individual data, for animals in population, for three or more molecular genetic markers for each selected quantitative trait locus;

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- c. a computer executable program capable of simultaneously evaluating the data in all databases and determining the relative informativeness for each of the molecular genetic markers for which data is provided;
 - d. a user interface including a data entry system, said user interface coupled to said computer and configured to allow the user to instruct the computer to access the available databases and use the computer program to generate output that includes a indication of the informativeness of each molecular genetic marker for which data was provided.
- 22. The system of claim 21 wherein the quantitative trait locus is selected from any locus know to be associated with a known trait.
- 23. The system of claim 21 wherein the quantitative trait locus is selected from any locus for traits selected from the group consisting of efficient growth traits, meat quality traits, reproduction traits, and health traits.
- 24. The system of claim 21 further comprising providing computer accessible database(s) containing individual data for animals in the population for at least one fixed effect; wherein the computer executable program is capable of simultaneously evaluating the data in all provided databases and ranking the animals in the population according to their respective estimated breeding value for each of the selected traits.
- 25. The system of claim 21 wherein the selected molecular genetic markers comprise a marker haplotype.
- 26. A method of identifying the molecular genetic marker(s) having the highest degree of informativeness for at least one quantitative trait locus (QTL), the method comprising.
 - a. selecting at least one trait for which an informative molecular genetic is desired;
 - b. providing database(s) comprising data for one or more quantitative trait locus (QTL) for each selected trait, for a plurality of animals in an animal population;
 - c. providing database(s) comprising data for three or more molecular genetic markers for each selected QTL for each selected trait, for a plurality of animals in an animal population;
 - d. using a computer program capable of performing a marker assisted best linear unbiased prediction to simultaneously analyze the data from all provided databases to calculate the informativeness of the provided markers;

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- e. identifying the marker(s) that is/are most informative for the selected trait(s).
27. The method of claim 26 further comprising providing databases comprising:
- i. data providing the pedigree for the animals in the animal population; and
 - ii. optionally, data for one or more fixed effects for the animals in the population;
- wherein the method also further comprises using the computer program capable to performing a marker assisted best linear unbiased prediction to simultaneously analyze the data from all provided databases to determine the informativeness of the selected markers and to calculate a ranking of the animals; wherein the animals are ranked according to their estimated breeding value (EBV) for the selected traits.
28. A method of evaluating an animal population's average genetic merit for a defined set of traits, wherein the defined traits comprise the animal's status for one or more quantitative trait locus (QTL) and at least three molecular genetic markers for each QTL, the animal's pedigree; the method comprising:
- a. selecting one or more traits for evaluation;
 - b. providing databases comprising:
 - i. data for one or more quantitative trait loci (QTL) for the animals in the population
 - ii. data for three or more selected molecular genetic markers for each QTL, for each selected marker for the animals in the population;
 - iii. data providing the pedigree for the animals in the population;
 - c. using a computer program capable of performing a marker assisted best linear unbiased prediction to simultaneously analyze the data from the provided databases to produce a ranking of the animals; wherein the animals are ranked according to their estimated breeding value (EBV) for the selected molecular genetic markers and, if provided, quantitative traits;
 - d. evaluating the EBVs to determine the animal population's average genetic merit for the defined set of characteristics.
29. A method of identifying optimal breeding pairs in an animal population to improve a previously selected characteristic in the population comprising:
- a. selecting one or more traits for improvement;
 - b. providing computer readable data for one or more quantitative trait locus for the selected traits;

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- c. providing computer readable data for at least three molecular genetic markers for each QTL for each selected trait; wherein the data indicates the genetic makeup of animals in the population, with respect to the molecular genetic marker;
 - d. providing computer readable data representing the pedigree for animals in the population;
 - e. using a computer program capable of performing a marker assisted best linear unbiased prediction to simultaneously analyze the data from the provided data to produce a ranking of the animals; wherein the animals are ranked according to their estimated breeding value (EBV) for the selected molecular genetic markers and, if provided, quantitative traits;
 - f. using the animals' ranks to identify the optimal breeding pairs in the population.
30. The method according to any one of claims 26 to 29 wherein the selected molecular genetic markers comprise a marker haplotype.
31. A method of enhancing one or more meat quality trait(s) in pigs, the method comprising:
- a) screening a plurality of pigs to identify the nature of one or more single nucleotide polymorphisms (SNPs) in the porcine PRKAG3 gene, wherein said SNP(s) is/are selected from the group consisting of: an A/G at position 51, A/G at position 462, A/G at position 1011, C/T at position 1053, C/T at position 2475, A/G at position 2607, A/G at position 2906, A/G at position 2994, and C/T at position 4506, wherein all numbering is according to the sequence of SEQ ID NO:1 and identifying those having a desired allele;
 - b) selecting those pigs identified as having a desired allele;
 - c) using the selected pigs as sires/dams in a breeding plan to produce offspring; wherein the offspring have an increase frequency of the desired allele.
32. The method of claim 31 wherein the presence or absence of the polymorphism is determined by a method selected from the group consisting of: DNA sequencing, restriction fragment length polymorphism (RFLP) analysis, heteroduplex analysis, single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), real time PCR analysis (TAQMAN®), temperature gradient gel electrophoresis (TGGE), primer extension, allele-specific hybridization, and INVADER® genetic analysis assays.

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33. The method of claim 31 wherein at least one meat quality trait is selected from the group consisting of increased pH and decreased 7-day purge.
34. A kit for detecting the nature of one or more polymorphisms in the porcine PRKAG3) gene; the kit comprising a means for detecting for detecting the polymorphism in the DNA and or RNA from the gene;
wherein the polymorphisms are selected from the group consisting of one or more of the following SNP(s): an A/G at position 51, A/G at position 462, A/G at position 1011, C/T at position 1053, C/T at position 2475, A/G at position 2607, A/G at position 2906, A/G at position 2994, and C/T at position 4506, wherein all numbering is according to the sequence of SEQ ID NO:1.
35. The kit of claim 34 whereby the polymorphism is detected by one or more of the following means of detection: DNA sequencing, restriction fragment length polymorphism (RFLP) analysis, heteroduplex analysis, single strand conformational polymorphism (SSCP), denaturing gradient gel electrophoresis (DGGE), polymerase chain reaction (PCR), real time PCR analysis (TAQMAN®), temperature gradient gel electrophoresis (TGGE), enzyme linked immunosorbent assay (ELISA) and other immunoassay;
wherein the kit comprises one or more of the following: a restriction endonuclease enzyme, a DNA polymerase, a reverse transcriptase, a buffer, deoxyribonucleotides, an oligonucleotide suitable for use as a DNA or RNA probe, an oligonucleotide suitable for use as a primer in DNA or RNA synthesis, a fluorescent marker, and an antibody.
36. An oligonucleotide suitable for use in a kit according to claim 35.
37. The oligonucleotide of claim 36 selected from primers comprising the sequence of any of the primers listed in Table 1 (SEQ ID NO:2-17).
38. The oligonucleotide of claim 36 selected from the group consisting of the primers provided in Table 1 (SEQ ID NO:2-17).

39. A method of screening animals to identify those more likely to produce offspring exhibiting at least one improved meat quality trait, the method comprising:
screening a plurality of pigs to identify the nature of one or more single nucleotide polymorphisms (SNPs) in the porcine PRKAG3 gene, wherein said SNP(s) is/are selected from the group consisting of: an A/G at position 51, A/G at position 462, A/G at position 1011, C/T at position 1053, C/T at position 2475, A/G at position 2607, A/G at position 2906, A/G at position 2994, and C/T at position 4506, wherein all numbering is according to the sequence of SEQ ID NO:1.
40. The method of claim 39 wherein the improved meat quality trait is selected from higher loin and/or ham pH and decreased 7-day purge or drip loss.
41. A pig offspring produced using any of the methods, systems, or kits of any one or more of the above claims.
42. A pig population produced using any of the methods, systems, or kits of any one or more of the above claims.
43. A method of increasing an animal population's average genetic merit, comprising:
- a. selecting one or more traits for which an improved genetic merit is desired;
 - b. selecting one or more quantitative trait locus (QTL) for each selected trait;
 - c. selecting one or more molecular genetic markers of interest for each QTL for each selected trait;
 - d. providing databases comprising:
 - i. genotype data for three or more molecular genetic markers for each selected trait, for a plurality of animals in the population;
 - ii. data providing the pedigree for each animal in the population;
 - iii. optionally, data for one or more fixed effects;
 - e. using a computer program capable of performing a marker assisted best linear unbiased prediction to simultaneously analyze the data from the provided databases to calculate a ranking of the animals; wherein the animals are ranked according to their estimated breeding value (EBV) for the selected molecular genetic markers and, if provided, quantitative traits.

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44. A system for increasing an animal population's average genetic merit for at one or more selected traits, the system comprising:
- a. a computer;
 - b. a computer accessible database providing data on one or more quantitative trait locus (QTL) for each selected trait;
 - c. a computer accessible database providing data, for animals in population, for one or more molecular genetic markers for each selected QTL for each selected trait;
 - d. a computer accessible database providing pedigree data for animals in the population;
 - e. optionally, a computer accessible database providing individual data for each animal in the population for at least one fixed effect;
 - f. a computer executable program capable of simultaneously evaluating the data in all databases and ranking the animals in the population according to their respective estimated breeding value for each of the selected traits;
 - g. a user interface including a data entry system, said user interface coupled to said computer and configured to allow the user to instruct the computer to access the available databases and use the computer program to generate output that includes a ranking of the animals according to their estimated breeding values and/or their individual estimated breeding values.
45. A method of identifying optimal breeding pairs in an animal population to improve a previously selected characteristic in the population comprising:
- a. selecting one or more traits for improvement;
 - b. providing computer readable data for one or more quantitative trait locus for the selected traits;
 - c. providing computer readable data for one or more molecular genetic markers for each QTL for each selected trait; wherein the data indicates the genetic makeup of animals in the population, with respect to the molecular genetic marker;
 - d. providing computer readable data representing the pedigree for animals in the population;
 - e. using a computer program capable of performing a marker assisted best linear unbiased prediction to simultaneously analyze the data from the provided data to produce a ranking of the animals; wherein the animals are ranked according to their

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- estimated breeding value (EBV) for the selected molecular genetic markers and, if provided, quantitative traits;
- f. using the animals' ranks to identify the optimal breeding pairs in the population.
46. A method of evaluating an animal population's average genetic merit for a defined set of traits, wherein the defined traits comprise the animal's status for one or more quantitative trait locus (QTL) and at least one or more molecular genetic markers for each QTL, the animal's pedigree; the method comprising:
- a. selecting one or more traits for evaluation;
 - b. providing databases comprising:
 - i. data for one or more quantitative trait loci (QTL) for the animals in the population
 - ii. data for one or more selected molecular genetic markers for each QTL, for each selected marker for the animals in the population;
 - iii. data providing the pedigree for the animals in the population;
 - b. using a computer program capable of performing a marker assisted best linear unbiased prediction to simultaneously analyze the data from the provided databases to produce a ranking of the animals; wherein the animals are ranked according to their estimated breeding value (EBV) for the selected molecular genetic markers and, if provided, quantitative traits;
 - d. evaluating the EBVs to determine the animal population's average genetic merit for the defined set of characteristics.